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CURRICULUM VITAE

Name: Michael Joseph Malasky

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Citizenship: United States

Education:

1999	B.A. (Biology Major), Hood College, Frederick, MD
1994	A.A. (Biological Laboratory Technician), Frederick Community College, Frederick, MD

Brief Chronology of Employment:

2005-Present Research Associate II, CORE Lab Manager, CCR/OD-Frederick, Contractor-SAIC-Frederick, Inc., NCI-Frederick Cancer Research and Development Center, Frederick, MD

Responsibilities include: I am Manager of the Core Genotyping Facility for the LGD. This involves a few techniques that the lab has picked up in the past few years. The First is with the implementation of high-throughput genotyping with the Illumina system. With this system they have many different techniques available to labs set for their specific needs. We utilize four of their techniques that fit into our general scheme for genotyping. I have learned these four systems and have implemented them into our system and also have learned the all the programs that have been involved with the genotyping and have helped set up our database to implement the tracking of samples and reagents. Illumina has four ways of genotyping samples. The first is the GoldenGate genotyping Assay which is a flexible, pre-optimized assay that uses a discriminatory DNA polymerase and ligase to interrogate 96, or from 384 to 1,536, SNP loci simultaneously. I have run this assay for around 100 plates for 96 samples which is a total of 9,600 samples for around 15 million genotypes. The second is the Infinium II assay which allows large-scale interrogation of variations in the human genome with using 550,000 to 660,000 SNP's. I have run this assay on 414 individual samples for a total of 228 million genotypes. The third is the Infinium Gemini assay which interrogates more than 1.1 million evenly distributed loci per sample. This assay targets high-value functional regions such as exons, the MHC, and ADME genes. This assay also contains copy number variation-targeted markers that target regions likely to contain undiscovered CNV's. This was a

small sample set of only 60 samples which yielded around 72 million genotypes. The forth is their iSelect assay which is a specific set of SNP's designed by the user from 6,000 SNP's up to 60,000 SNP's which was used to look at a specific area of interest. I ran this assay for 7 plates and helped out another lab with the analysis and training of this iSelect assay.

The second major high-throughput assay that we use is the Affymetrix Genome-Wide Human SNP Array 6.0. This is a single array that features more than 1.8 million markers for genetic variation, including more than 906,600 SNP's and more than 946,000 additional probes for the detection of copy number variations. We have completely run a phase 1 of 2,000 plus HIV patients and are currently running phase 2 of 5,000 to 6,000 samples.

Even with all of this going on I still have to maintain all of the DNA stocks from all of the various cohorts that are available to the LGD. With this responsibility, I maintain the distribution of DNA to all of the labs of the LGD, I help to maintain DNA plates that are designed to aide researchers for specific disease interests and I am in charge of DNA extractions for the LGD in which outside collaborators send various samples for DNA extractions. I have extracted DNA from various sources such as tissue, buffy coat, whole blood, TES blood, cell pellets, and buccal swabs in both swab form and mouthwash. I also oversee and work a lot on the ABI 3730XL which is the main sequencing machine in the CORE lab. This sequencer is utilized by several different labs and we use several programs such as AMPure and CleanSeq to get the samples ready for sequencing. We are currently running the sequencer non-stop and typically run 100 plus sequences a week.

1999-2005 Sr. Research Technician, Laboratory of Genomic Diversity (LGD), Basic Research Program, SAIC-Frederick, Inc., NCI-Frederick Cancer Research and Development Center, Frederick, MD

Responsibilities include: I am the supervisor of the Core Genotyping Facility for the Laboratory of Genomic Diversity. This involves the amplification and analysis of twelve major sites. These sites include CCR5, CCR2, SDF-1, CCR5 Promoter, IL-10, IFNG-179, Rantes 28, Rantes 403, Rantes In1, CX3CR1249, CX3CR1280, and MCP1364. These are done when any of the groups Principal Investigators get in samples that need these sites done. I am the only person that does these sites within the LGD. These samples are then entered into a computer-based system called File-maker and from here our computer service technicians analyze them. I also maintain all of the DNA stocks from all of the various cohorts that are available to the LGD. With this responsibility, I maintain the distribution of DNA to all of the labs of the LGD, I help to

maintain DNA plates that are designed to aide researchers for specific disease interests and am in charge of DNA extractions for the LGD in which outside collaborators send various samples for DNA extractions. I have extracted DNA from various sources such as tissue, buffy coat, whole blood, TES blood, cell pellets, and buccal swabs in both swab form and mouthwash. The Core genotyping facility has just converted to a high throughput system, which involves two new techniques from two different companies. One being ParAllele which we have done a beta test for on approximately 2,500 patients for 3,000 +/- SNP's. This is done by using florescently tagged probes that are on a chip and hybridizing the samples directly onto the chip, then running them through a special machine to analyze the probes. Secondly is a system developed by Illumina in which samples are hybridized onto approximately 50,000 fiber optic cables, which are tagged with 1,536 probes repeated in random areas so that the error rate is greatly reduced. This is then run through a dedicated machine and then the operator analyzes all 1,536 probes.

1994-1999 Research Technician/Radiation Safety Officer, Intramural Research Support Program, NCI-Frederick Cancer Research and Development Center, Frederick, MD

Responsibilities include: As a Research Technician, I performed individual studies on large families of study. With these samples I tested microsattelites located on various locations on chromosome 6 to determine gene mutation and genetic crossovers within each family. I have worked on several types of families such as CEPH, IDDM, Leppert, and Huntington patients to determine the frequency of genetic crossovers. These tests are done by the PCR process and then run on sequencing gel electrophoresis to determine family unity and conformity.

As a Research Technician, I was given the responsibility of becoming the Radiation Safety Officer of Program 95-01. With the responsibility of this position, I monitored all ordering and record keeping of all radio nucleotide isotopes within the lab, all of the personal in my program for handling and usage of all isotopes within the lab and I maintained all employee records of biological assays and training of all personal coming into and out of the program. Along with this responsibility, I monitored all of rooms under my program for any trace of possible contamination. Since my start in 1995, there have been no traces of any area of contamination or any major spills of radioactive materials.

1992-1994 Biological Laboratory Technician (B.L.T.), Intramural Research Support Program, NCI-Frederick Cancer Research and Development Center, Frederick, MD

Responsibilities included: As a BLT I preformed certain tasks such a Polymerase chain reactions (PCR) on selected family cohorts of study for HLA class II typing. Also, on these samples I preformed single strand conformation polymorphism gel electrophoresis to determine family structure and uniformity of the patients. I preformed hybridization and dot-blot tests on these cohorts. I aided and preformed DNA extractions from cell pellets to obtain workable DNA.

Research Interests:

CCR5 Genotyping, HIV research, and other disease associations due to genetic markers, High-throughput genotyping with new techniques, DNA extractions, Cell culture, Database work, and genotyping analysis

Publications:

1. Stephens, J. C., Reich, D. E., Goldstein, D. B., Shin, H. D., Smith, M. W., Carrington, M., Winkler, C., Huttley, G. A., Allikmets, R., Schriml, L., Gerrard, B., Malasky, M., Ramos, M. D., Morlot, S., Tzetis, M., Oddoux, C., diGiovine, F. S., Nasioulas, G., Chandler, D., Aseev, M., Hanson, M., Kalaydjieva, L., Glavac, D., Gasparini, P., Kanavakis, E., Claustres, M., Kambouris, M., Ostrer, H., Duff, G., Baranov, V., Sibul, H., Metspalu, A., Goldman, D., Martin, N., Duffy, D., Schmidtke, J., Estivill, X., O'Brien, S. J. and Dean, M.: Dating the origin of the CCR5-delta32 AIDS-resistance allele by the coalescence of haplotypes. Amer. J. Hum. Genet. 62: 1507-1515, 1998.

2. Cullen, M., Malasky, M., Harding, A. and Carrington, M.N.: High-Density Map of Short Tandem Repeats Across the Human Histocompatibility Complex.: Immunogenetics. 54 (12): 900-910, October 2002.

3. Smith MW, Patterson N, Lautenberger JA, Truelove AL, McDonald GL, Waliszewska A, Kessing BD, Malasky MJ, Scafe C, Le E, De Jager PL, Mignault AA, Yi Z, De The G, Essex M, Sankale JL, Moore JH, Poku K, Phair JP, Goedert JJ, Vlahov D, Williams SM, Tishkoff SA, Winkler CA, De La Vega FM, Woodage T, Sninsky JJ, Hafler DA, Altshuler D, Gilbert DA, O'Brien SJ, Reich D.: A high-density admixture map for disease gene discovery in African Americans. Amer. J. Hum. Genet. 74(5): 1001-1013, 2004

In Press:

1. Sher L. Hendrickson, James Lautenberger, Leslie Chinn, Michael Malasky, Efe Segin, Lawrence A. Kingsley, James J. Goedert, Gregory D. Kirk, Edward D. Gomperts, Susan P. Buchbinder, Jennifer Troyer, and Stephen J. O'Brien.: Genetic Variants in Nuclear-encoded mitochondrial genes influence AIDS progression.

2. Leslie W Chinn, Ph.D.; Minzhong Tang; Bailey D Kessing; James A Lautenberger; Jennifer L Troyer; Michael J Malasky; Carl McIntosh; Gregory D Kirk; Steven M Wolinsky; Susan P Buchbinder; Edward D Gomperts; James J Goedert; Stephen J O'Brien.: Genetic associations of variants in genes encoding HIV-dependency factors (HDFs) required for HIV-1 infection.

3. Jennifer L. Troyer, Ph.D.; George W Nelson, Ph.D.; James A Lautenburger, Ph.D.; Leslie Chinn, Ph.D.; Carl McIntosh; Randall C Johnson; Efe Sezgin, Ph.D.; Bailey Kessing; Michael Malasky; Sher Hendrickson, Ph.D.; Guan Li; Minzhong Tang, Ph.D.; Ping An, Ph.D.; Cheryl A Winkler, Ph.D.; Sophie Limou; Sigrid Le Clerc; Olivier Delaneau, Ph.D.; Jean-François Zagury, M.D.; Hanneke Schuitemaker, Ph.D.; Daniëlle van Manen; Jay H Bream, Ph.D.; Edward D Gomperts, M.D.; Susan Buchbinder, M.D.; James J Goedert, M.D.; Gregory D Kirk, Ph.D.; Stephen J O'Brien, Ph.D.: PARD3B-based AIDS restriction discovered by genome-wide association study

Abstracts:

1. Carrington, M., Marti, D., Malasky, M., Barcellos, L., Wade, J., Awdeh, Z. and Truedsson, L.: Mapping Disease Loci Within the MHC by Typing Microsatellite Loci. 22nd Annual Meeting of the American Society for Histocompatibility and Immunogenetics, October 1996.